

FIG. 1

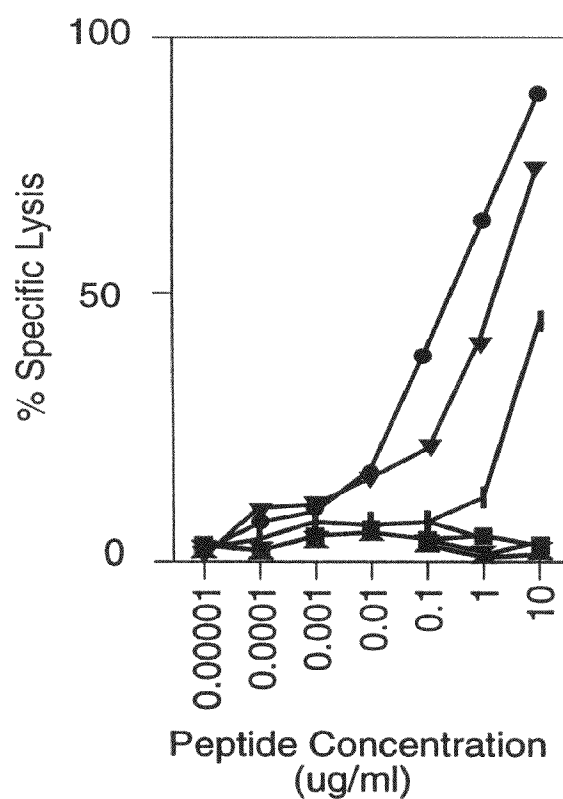
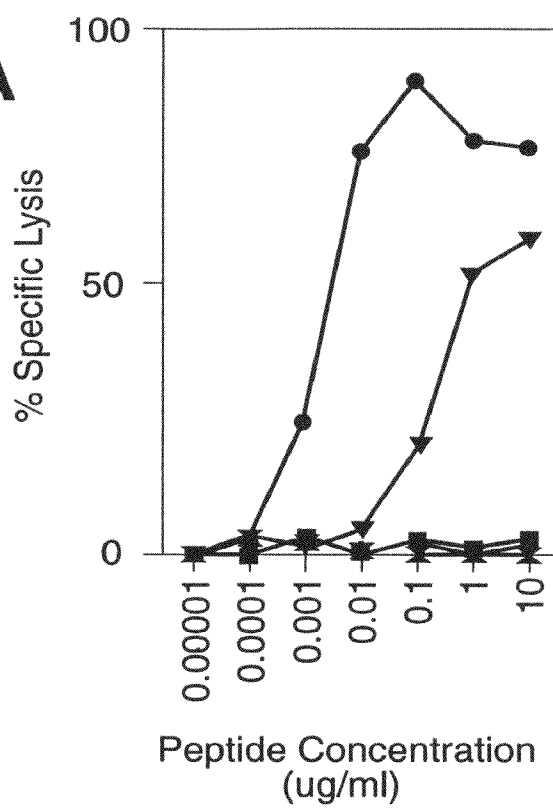
1	AGCAGACAGAGGACTCTCATTAAAGGAAGG	TGTCCTGTGCCCCCTGACCCCTACAAGATGCCA	59
		MetPro	2
60	AGAGAAAGATGCTCAGCTTCTATCTATGGTTAC	CCCAAGAAAGGGGCACGGCCACTCTTTACACC	119
3	ArgGluAspAlaHisPheIleTyrGlyTyr	ProLysLysGlyHisGlyHisSerTyrThr	22
120	ACGGCTGAAGAGGCGCTGGGATCGGCATC	CTGACAGTGAATCCTGGGAGTCTTACTGCTC	179
23	ThrAlaGluGluAlaAlaGlyIleGlyIle	LeuThrValIleLeuGlyValLeuLeuLeu	42
180	ATCGGCTGTTGGTATTGTAGAACGAAAT	GGATACAGAGCCTTGATGCATAAAAAGTCTT	239
43	IleGlyCysTrpTyrCysArgArgArgAsn	GlyTyrArgAlaLeuMetAspLysSerLeu	62
240	CATGTTGGCACTCAATGTGCCTTAACAAGA	AGATCCCCCACAAAGAAGGGTTTGATCATCGG	299
63	HisValGlyThrGlnCysAlaLeuThrArg	ArgCysProGlnGluGlyPheAspHisArg	82
300	GACAGCAAAGTGTCCTCTTCAAGAGAAAAAC	TGTGAACCTGTGGTTCCCAATGCTCCACCT	359
83	AspSerLysValSerLeuGlnGluLysAsn	CysGluProValValProAsnAlaProPro	102
360	GCTTATGAGAAAACTCTCTGCAGAACAGTCA	CCACCACCTTATTACCTTAAGAGCCAGCG	419
103	AlaTyrGluLysLeuSerAlaGluGlnSer	ProProProTyrSerPro	
420	AGACACCTGAGACATGCTGAAATTATTCT	CTCACACTTTTGTCTGAATTTAATACAGAC	479
480	ATCTAATGTTCTCCTTTGGAATGGTGAGG	AAAAATGCAAGCCATCTCTAATAATAAGTC	539
540	AGTGTTAAAAATTTTAGTAGGTCCGCTAGCA	GTAATAATCATGTGAGGAAAATGATGAGAAA	599
600	TATTAATTTGGGAAAACTCCATCAATAAAT	GTTGCAATGCATGATACTATCTGTGCCAGA	659
660	GGTAATGTTAGTAAATCCATGGTGTTATTT	TCTGAGAGACAGAAATCAAGTGGGTATTCT	719
720	GGGGCCATCCAAATTTCTCTTTACTTGAAAT	TTGGCTAATAACAAAACATGTCAGGTTTTCG	779
780	AACCTTGACCGACATGAACGTACACAGAA	TTGTTCCAGTACTATGGAGTGTCACAAAAG	839
840	GATACTTTTACAGGTTAAGACAAAAGGTTG	ACTGGCTATTTATCTGTATCAAGAACATGT	899
900	CAGCAATGTCCTTTGTGCTCTAAATTTCT	ATTATACTACAATAATATATTGTAAGATC	959
960	CTATAGCTCTTTTGTGATGGAGTTT	CGCTTTTGTGCCCCAGCAATCTCCTGCCATTG	1019
1020	GCGCGATCTTGGCTACCATAACTCCGCC	TCCCAGGTTCAAGCAATCTCCTGCCATTAG	1079
1080	CCTCCTGAGTAGCTGGGATTACAGGCGTGC	GCCACTATGCCCTGACTAATTTTGTAGTTT	1139
1140	AGTAGAGACGGGTTTCTCCATGTTGGTCA	GGCTGGTCTCAAACTCCTGACCTCAGGTGA	1199
1200	TCTGCCCGCCTCAGCCTCCCAAAGTCTGG	AATTACAGGCTGAGCCACCAAGCTGGCT	1259
1260	GGATCCTATATCTTAGGTAAGACATATAAC	GCAGTCTAATTACATTTCACTCAAGGCTC	1319
1320	AATGCTATTCTAACTAATGACAAAGTATTT	CTACTAAACCAATAATTTGGTAGAAGGATT	1379
1380	AAATAAGTAAAGCTACTATGTACTGCCTT	AGTGCTGATGCTGTGTACTGCTTAAATG	1439
1440	TACCTATGGCAATTTAGCTCTCTTGGGTTT	CCAAATCCCTCTCACAAAGATGTGCAGAA	1499
1500	AAATCATAAAGGATCAGAGATTCTGAAAAA	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1559

5844075

08/4/17

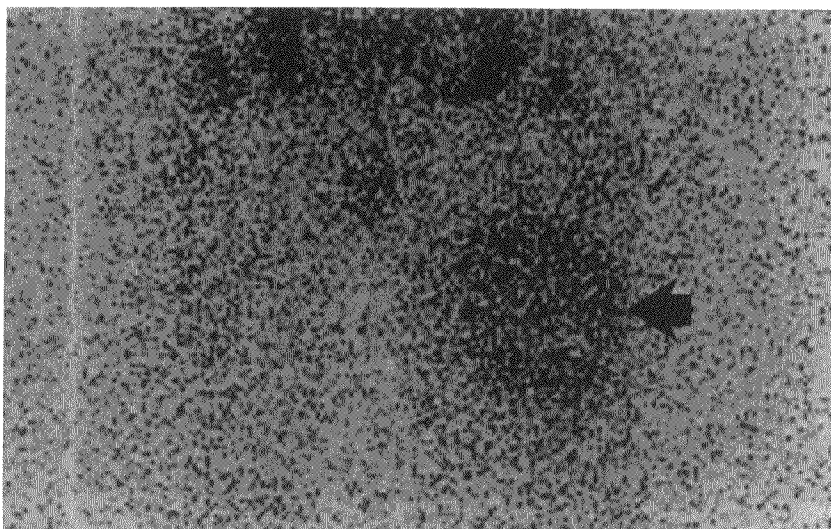
530 326

**FIG. 2A**

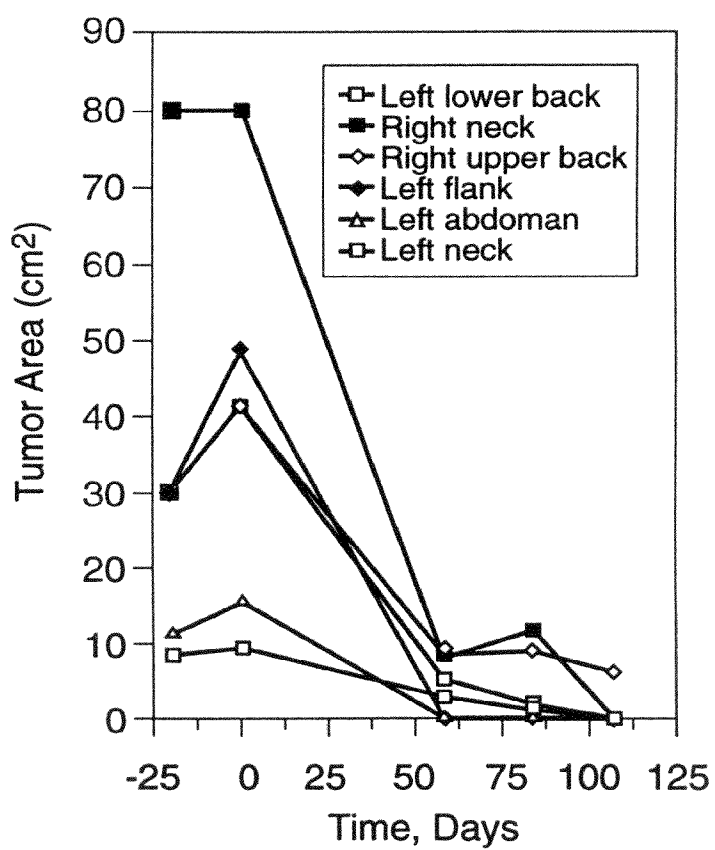


**FIG. 2B**

**FIG. 3A**



**FIG. 3B**



## FIG. 4A

GTCGACGGCC	ATTACCAATC	GCGACCGGGA	AGAACACAAT	40
GGATCTGGTG	CTAAAAAGAT	GCCTTCTTCA	TTTGGCTGTG	80
ATAGGTGCTT	TGCTGGCTGT	GGGGGCTACA	AAAGTACCCA	120
GAAACCAGGA	CTGGCTTGGT	GTCTCAAGGC	AACTCAGAAC	160
CAAAGCCTGG	AACAGGCAGC	TGTATCCAGA	GTGGACAGAA	200
GCCCAGAGAC	TTGACTGCTG	GAGAGGTGGT	CAAGTGTCCC	240
TCAAGGTCAG	TAATGATGGG	CCTACACTGA	TTGGTGCAAA	280
TGCCTCCTTC	TCTATTGCCT	TGAACTTCCC	TGGAAGCCAA	320
AAGGTATTGC	CAGATGGGCA	GGTTATCTGG	GTCAACAATA	360
CCATCATCAA	TGGGAGCCAG	GTGTGGGGAG	GACAGCCAGT	400
GTATCCCCAG	GAAACTGACG	ATGCCTGCAT	CTTCCCTGAT	440
GGTGGACCTT	GCCCATCTGG	CTCTTGGTCT	CAGAAGAGAA	480
GCTTTGTTTA	TGTCTGGAAG	ACCTGGGGCC	AATACTGGCA	520
ATTTCTAGGG	GGCCCAGTGT	CTGGGCTGAG	CATTGGGACA	560
GGCAGGGCAA	TGCTGGGCAC	ACACACCATG	GAAGTGA CTG	600
TCTACCATCG	CCGGGGATCC	CGGAGCTATG	TGCCTCTTGC	640
TCATTCCAGC	TCAGCCTTCA	CCATTACTGA	CCAGGTGCCT	680
TTCTCCGTGA	GCGTGTCCCA	GTTGCGGGCC	TTGGATGGAG	720
GGAACAAGCA	CTTCCTGAGA	AATCAGCCTC	TGACCTTTGC	760
CCTCCAGCTC	CATGACCCCA	GTGGCTATCT	GGCTGAAGCT	800
GACCTCTCCT	ACACCTGGGA	CTTTGGAGAC	AGTAGTGGAA	840
CCCTGATCTC	TCGGGCACTT	GTGGTCACTC	ATACTTACCT	880
GGAGCCTGGC	CCAGTCACTG	CCCAGGTGGT	CCTGCAGGCT	920
GCCATTCCCTC	TCACCTCCTG	TGGCTCCTCC	CCAGTTCCAG	960
GCACCACAGA	TGGGCACAGG	CCAACTGCAG	AGGCCCCTAA	1000
CACCACAGCT	GGCCAAGTGC	CTACTACAGA	AGTTGTGGGT	1040
ACTACACCTG	GTCAGGCGCC	AACTGCAGAG	CCCTCTGGAA	1080
CCACATCTGT	GCAGGTGCCA	ACCACTGAAG	TCATAAGCAC	1120

## FIG. 4B

TGCACCTGTG	CAGATGCCAA	CTGCAGAGAG	CACAGGTATG	1160
ACACCTGAGA	AGGTGCCAGT	TTCAGAGGTC	ATGGGTACCA	1200
CACTGGCAGA	GATGTCAACT	CCAGAGGCTA	CAGGTATGAC	1240
ACCTGCAGAG	GTATCAATTG	TGGTGCTTTC	TGGAACCACA	1280
GCTGCACAGG	TAACAACCTAC	AGAGTGGGTG	GAGACCACAG	1320
CTAGAGAGCT	ACCTATCCCT	GAGCCTGAAG	GTCCAGATGC	1360
CAGCTCAATC	ATGTCTACGG	AAAGTATTAC	AGGTTCCCTG	1400
GGCCCCCTGC	TGGATGGTAC	AGCCACCTTA	AGGCTGGTGA	1440
AGAGACAAGT	CCCCCTGGAT	TGTGTTCTGT	ATCGATATGG	1480
TTCCTTTTCC	GTCACCCTGG	ACATTGTCCA	GGGTATTGAA	1520
AGTGCCGAGA	TCCTGCAGGC	TGTGCCGTCC	GGTGAGGGGG	1560
ATGCATTTGA	GCTGACTGTG	TCCTGCCAAG	GCGGGCTGCC	1600
CAAGGAAGCC	TGCATGGAGA	TCTCATCGCC	AGGGTGCCAG	1640
CCCCCTGCCC	AGCGGCTGTG	CCAGCCTGTG	CTACCCAGCC	1680
CAGCCTGCCA	GCTGGTTCTG	CACCAGATAC	TGAAGGGTGG	1720
CTCGGGGACA	TACTGCCTCA	ATGTGTCTCT	GGCTGATACC	1760
AACAGCCTGG	CAGTGGTCAG	CACCCAGCTT	ATCATGCCTG	1800
GTCAAGAAGC	AGGCCTTGGG	CAGGTTCCGC	TGATCGTGGG	1840
CATCTTGCTG	GTGTTGATGG	CTGTGGTCCT	TGCATCTCTG	1880
ATATATAGGC	GCAGACTTAT	GAAGCAAGAC	TTCTCCGTAC	1920
CCCAGTTGCC	ACATAGCAGC	AGTCACTGGC	TGCGTCTACC	1960
CCGCATCTTC	TGCTCTTGTC	CCATTGGTGA	GAACAGCCCC	2000
CTCCTCAGTG	GGCAGCAGGT	CTGAGTACTC	TCATATGATG	2040
CTGTGATTTT	CCTGGAGTTG	ACAGAAACAC	CTATATTTCC	2080
CCCAGTCTTC	CCTGGGAGAC	TACTATTAAC	TGAAATAAAT	2120
ACTCAGAGCC	TGAAAAAAAA	TAAAAAAAAA	AAAAAAAAAA	2160
AAAAAAAAAA	AA			2172

FIG. 5A

1

MDLV

LKRC

LL

HLA

VIGALLA

VGAT

KVPR

NQ

DWL

GVSR

QLR

TKAW

NRQL

YP

51

EWTE

AQRL

DC

WRGG

QVSL

KV

SND

GPT

LIGA

NASF

SIAL

NF

PGSQ

KVLP

DG

101

QVIW

VNNT

II

NGSQ

VWGG

QP

VYP

QET

DDAC

IFPD

GGPC

PS

GSWS

QKR

SFV

151

YVWK

TWGQ

YW

QFLG

GPVS

GL

SIGT

GRAM

LG

THTM

EVT

VYH

RRGS

RSY

VPL

201

AHSS

SAFT

TIT

DQVP

FSVS

SVS

QLRA

LDGG

NK

HFLR

NQPL

TF

ALQL

HDPS

GY

251

LAEAD

LSYTW

DFGD

SSGT

LI

SRAL

VVTH

TY

LEPG

PVTA

QV

VLQA

AIPL

TS

301

CGSS

PVPG

TT

DGHR

P

TAEAP

NTTA

GQVP

TT

EVVG

TTPG

QA

PTAE

PSGT

TS

351

VQVP

TTEVIS

TAPV

QMPT

A

STGM

TPEK

VP

VSEV

MGT

T

LA

EMST

PEAT

GM

401

TPAE

VSIV

VL

SGTT

AAQV

TT

TEWV

ETTARE

LPIPE

PEGP

D

ASSI

MSTES

I

451

TGSL

G

PLLDG

TATL

R

LVKR

Q

VPLD

CVLY

RY

GSFS

VTLD

IV

QGIE

SAEIL

Q

501

AVPS

GEGDA

F

ELTV

SCQG

GL

PKEA

CMEISS

PGCQ

PPAQ

RL

CQPV

LPSP

PAC

551

QLVL

HQIL

KG

SGTY

CLNV

S

LADT

NSLAV

V

STQL

IMPG

QE

AGLG

QVPL

LIV

601

GILL

V

MAVV

LASLI

YRRRL

MKQD

FSVP

QL

PHSS

SHWL

RRL

PRIF

CSCPI

G

651

ENS

PLLS

GQQ

V

FIG. 5B

Pme117

M-----V-----Q-----P-----VPGILLT-----LLSGQQV

ME20

M-----V-----Q-----L-----.....

gp100

M-----V-----Q-----L-----.....

cDNA25FL

M-----F-----Q-----L-----.....

cDNA25TR

Q-----L-----.....PPQWAAGLSTLI

1

162

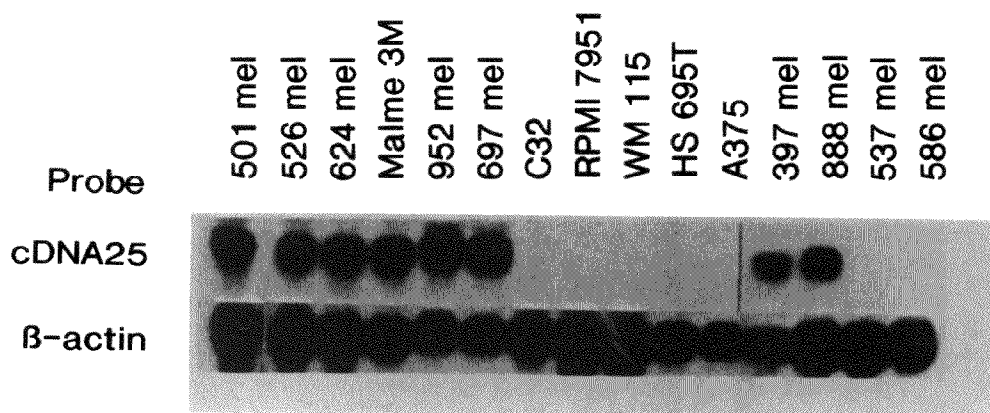
236

274

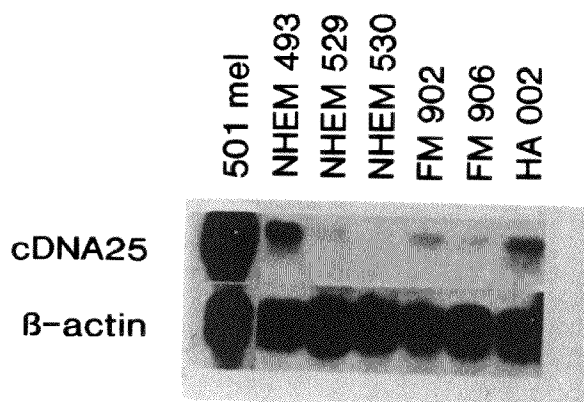
588

649

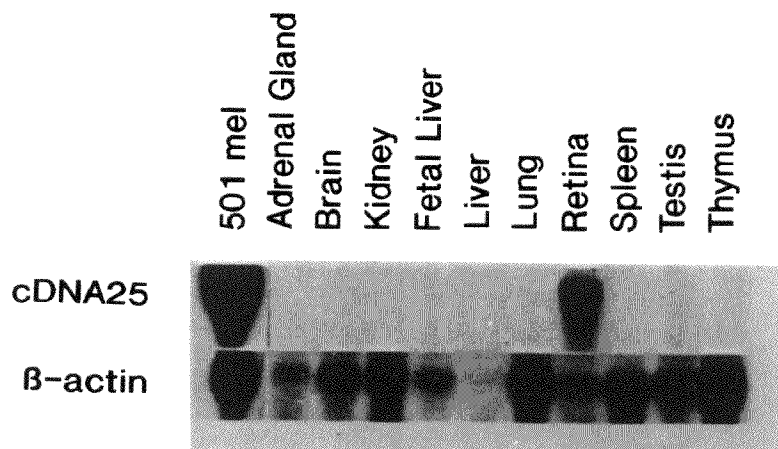
**FIG. 6A**



**FIG. 6B**



**FIG. 6C**



# FIG. 7A

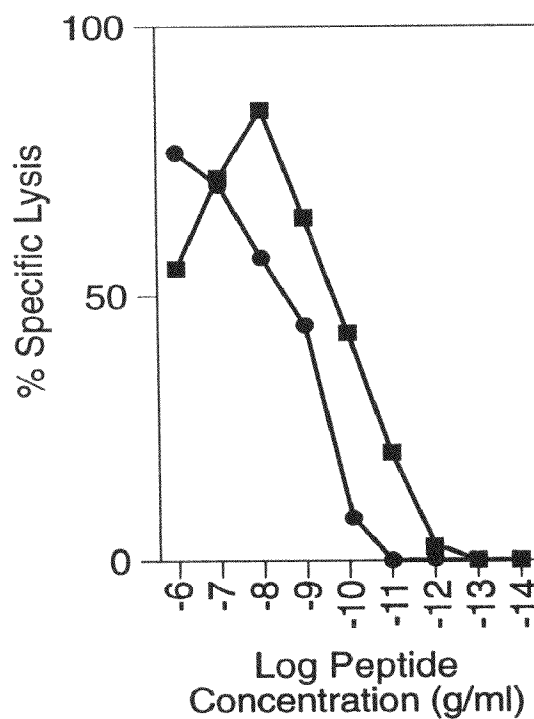
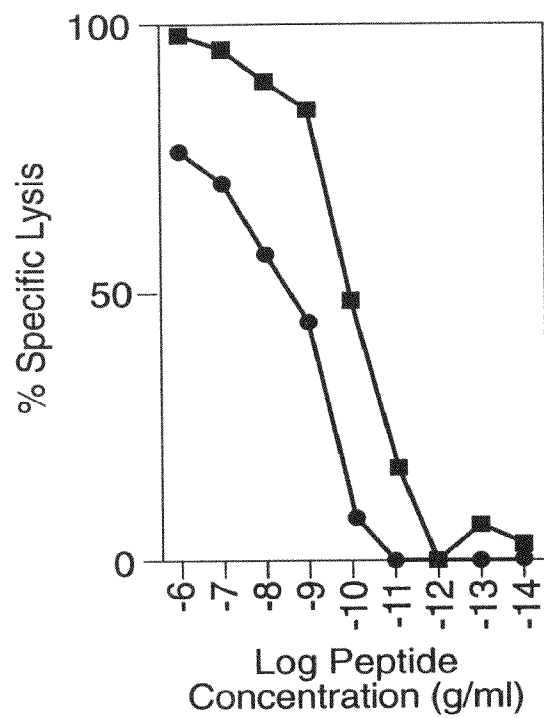
1	MDLVLRCLL	HLAVIGALLA	VGATKVP RNQ	DWLGVS RQLR	TKAWN RQLYP
	D3-----	-----	-----	-----	-----
	D5-----	-----	-----	-----	-----
	D4-----	-----	-----	-----	-----
	C4-----	-----	-----	-----	-----
51	EWTEAQLDC	WRGGQVSLKV	SNDGPTLIGA	NASF SIALNF	PGSQKVL PDG
	D3-----	-----	-----	-----	-----
	D5-----	-----	-----	-----	-----
	D4-----	-----	-----	-----	-----
	C4-----	-----	-----	-----	-----
101	QVIWVNNTII	NGSQVWGGQP	VYPQETDDAC	IFPDGGPCPS	GSWSQKRSFV
	D3-----	-----	-----	-----	-----
	D5-----	-----	-----	-----	-----
	D4-----	-----	-----	-----	-----
	C4-----	-----	-----	-----	-----
151	YVWKTWGQYW	QVLGGPV SGL	SIGTGRAMLG	THTMEVTVYH	RRGSR SYVPL
	D3----D3	-----	-----	-----	-----
	D5-----	---D5	-----	-----	-----
	D4-----	-----	-----	-----	-----D4
	C4-----	-----	-----	-----	-----
201	AHSSSAFTIT	DQVPFSVSVS	QLRALDGGNK	HFLRNQPLTF	ALQLHDPSGY
	C4-----	-----	-----	-----	-----
				25TR-----	-----
251	LAEADLSYTW	DFGDSSGTLI	SRALVVTHTY	LEPGPVTAQV	VLQAAIPLTS
	C4-----	-----C4	-----	-----	-----
	25TR-----	-----	-----	-----	-----
301	CGSSPVP GTT	DGHRPTAEAP	NTTAGQVPTT	EVVGTT PGQA	PTAEP SGTTs
	25TR-----	-----	-----	-----	-----
351	VQVPTTEVIS	TAPVQMPTAE	STGMTPEKVP	VSEVMGTTLA	EMSTPEATGM
	25TR-----	-----	-----	-----	-----
401	TPAEVSIVVL	SGTTAAQVTT	TEWVETTARE	LPIPEPEGPD	ASSIMSTESI
	25TR-----	-----	-----	-----	-----
451	TGSLG PLLDG	TATLRLVKRQ	VPLDCVLYRY	GSFSVTLDIV	QGIESAEILQ
	25TR-----	-----	-----	-----	-----
501	AVPSGEGDAF	ELTVSCQGGL	PKEACMEISS	PGCQPPAQRL	CQPVLPSPAC
	25TR-----	-----	-----	-----	-----
551	QLVLHQILKG	SGSTYCLNVS	LADTNSLAVV	STQLIMPGQE	AGLGQVPLIV
	25TR-----	-----	-----	-----	-----
601	GILLVLM AVV	LASLIYRRRL	MKQDFSVPQL	PHSSSHWLRL	PRIFCSCPIG
	25TR-----	-----	-----	-----	-----
651	ENSPLL SGQQ	V			
	25TR-----	-25TR			



**FIG. 7B**

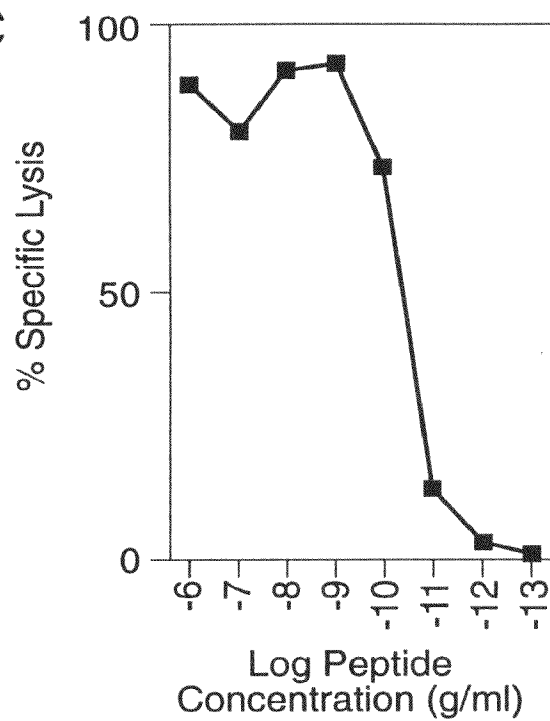
DNA fragment	TIL				
	620-1	620-2	660-1	1143	1200
D3	-	-	-	-	-
D5	-	+	-	-	+
D4	-	+	-	-	+
C4	+	+	+	+	+
25TR	-	-	+	+	+

**FIG. 8A**



**FIG. 8B**

**FIG. 8C**



**FIG. 8D**

